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GENE ACTION STUDIES IN *BRASSICA RAPA* FOR SEED YIELD RELATED TRAITS

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Pakistan is deficient in production of edible oil. Domestic edible oil production needs to be increase. *Brassica rapa* can be a better source for filling the gap between consumption and production of oil production, due to its yellow seeded nature. The goal of this study is to gather and develop information on genetics of different plants and seed yield related traits of *Brassica rapa*. A randomized complete block design is used for estimation of the genetic expression on seed yield related traits using four lines (UAF-11, Toria, BSA and TP-124-1) in diallel fashion. Statistical analysis was analyzed using Statistix 8.1. The presence of partial dominance type of gene action and the absence of epistasis was observed. Partial dominant gene action was observed in all traits. Direction of dominance was more frequent towards better parents except seed yield per plant. The number of recessive genes were more than that of dominant genes except number of seeds/siliqua. Maternal effects were observed in all traits. This study shows that UAF-11 is the best parent for *Brassica rapa* because it has the maximum dominant genes for almost all traits and can be utilized in future breeding efforts.
Keywords*:* Diallel, dominance, edible oil, genetic variability, scaling test.

INTRODUCTION

Pakistan is deficient in production of edible oil. About 34% (0.612 million) of domestic edible oil is produced in comparison to the total requirement (2.35 million tons) of edible oil. Pakistan expended Rs.153.3 billion in 2013 on importation of edible oil. Edible oil production from rapeseed is 0.051 million tons (8.34%). Industrial usage (Cosmetics, paints and other products) was estimated to be 10% of total requirement (Govt. of Pakistan, 2012-2013).

It is needed to focus on oilseeds crops due to increasing gap because of increasing human population and vegetable usage. After cottonseed, rapeseed and mustards (Brassica oilseeds) crops are largest producers of vegetable oil in Pakistan. *Brassica rapa* (syn *campestris)* is an important oilseed crop of the world and belongs to order Brassicales and Brassicaceae family. It has an oil content ranging from 35% to 46 % (Kumar *et al.,* 2011) which covers an area of 0.183 million hectares as at 2013. The major crops wheat and rice was 8.693 million and 2.311 million hectares respectively. The share of remaining oilseed crops sunflower and soybean is very low in local production of edible oil (Govt. of Pakistan, 2012-2013). Currently, existing *B. rapa* varieties are have limitations such as a low yield, aphid attack, white rust of crucifer, low percentage of better quality oil, and shattering at maturity. Additionally, lodging problem due to winds and rains is also a major limitation (Mumtaz *et al*., 2014). Farmers are also reluctant to grow it due to problems in its economic return but with such varieties of high yielding and short duration, its area and production can be increases and farmers can be attracted towards it. As, yellow seeded varieties have potential of more oil (Kumar *et al.,* 2011). So it is needed to breed high yielding seeded varieties for increasing oil yield and quality. *B. rapa* has a maturity period of almost 100 to 140 days. It is needed to develop varieties with high yielding capacity, better oil quality, and matures quickly; as early as 60 to 90 days to fit in the cropping systems. This research seeks to gather and develop information on genetics of different plant and seed yield related traits of *Brassica rapa.* We anticipate the findings from our research would be helpful to researchers and farmers to improve *Brassica rapa* seeds, oil quality, and its production.

MATERIALS AND METHODS

This research was conducted at the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad between October 2013 to February 2014. Four accessions of *Brassica rapa* were sown namely UAF-11, BSA, Toria and TP-124-1 and were crossed in diallel fashion in all possible combinations including self and reciprocal crosses. All the agronomic practices (i.e hoeing, irrigation, pest and weed control) recommended for *Brassica rapa* were followed throughout growing season.

All the necessary precautionary measures such as sterilization of emasculation instruments, covering of emasculated, and

pollinated flower were conducted. This was done to avoid the contamination of the genetic material (pollen and ovary) during time of crossing.

Twelve hybrids of *B. rapa* along with their parents were sown in November, 2013 in the field of department of Plant Breeding and Genetics. The design of experiment was randomized complete block design. Randomization is done using lottery method.

Traits studied**:** Data was collected on the plant (Plant Height) and seed yield related traits (Seed volume, 100 seed weight, No. of siliquae/primary branches of plant, No. of siliquae/secondary branches of Plant, total No. of siliquae per plant, seed yield per plant, siliqua length and No. of seeds per siliqua

Statistical Analysis**:** Statistical analysis was done following Steel *et al.,* (1997) and diallel analysis will be done following Hayman (1954) and Jinks (1954).

RESULTS AND DISCUSSIONS

Hayman and Jinks Model**:** The mean values of all plant traits were measured and statistically analyzed according to Steel *et al.,* (1997). The results of this ANOVA can be seen in the Table 1. The combined ANOVA (Table 1) showed that all the traits (Seed Volume,100 seed weight, siliqua length, seeds per siliqua, seed yield per plant, No. of siliquae per plant, No. of siliquae/Primary branches of Plant, No. of siliquae/Secondary branches of Plant, plant height) have significant differences for their mean squares (α=0.01). Replication in all traits has non-significant differences for its mean squares (α=0.05) which means that it has no effect in controlling variation. Results of combined ANOVA represented high significant variability which means that Hayman (1954) and Jinks (1954) simple additive model and heterosis analysis can be used for analyzing the data. Adequacy of Hayman (1954) and Jinks (1954) was determined through scaling test i.e Joint regression analysis and regression coefficient (b) of every trait. These are given in the Table 2.

For complete suitability of additive dominance mode these conditions are necessary, b=0 is significant, b-1 is non-significant, Wr+Vr is significant and Wr-Vr is non-significant and if one of them deviate then additive dominance model is partially suitable for them and if two of them deviate then additive dominance model is not suitable for them. Significant difference between the array (Wr + Vr) and non-significant difference within the array (Wr-Vr) for seed volume, 1000 seed weight, No. of siliqua/ primary branch of plant and siliqua length showed inter-allelic interaction in the inheritance of these characters, which means additive dominance model was good for these characters, while significant differences between the array (Wr + Vr) and significant difference within the array (Wr – Vr) for plant height, No. of siliquae/ secondary branches of plant, total No. of siliquae/ plant, seed yield/ plant and No. of seeds/ siliqua showed that additive dominance model was partially suitable for these. Regression coefficient (b) should deviate from zero as well as from unity according to Hayman (1954), it was observed from scaling tests that regression coefficient (b) for

Table 1: **Combined ANOVA for different traits in *Brassica rapa.***

Traits	Replication (DF=1)	Genotype (DF=15)	Error (DF=15)
Plant Height	10.26	544.32**	14.95
Seed Volume	0.01	1.29**	0.01
1000 Seed Weight	0.01	1.65**	0.01
No. of siliqua/ Primary branch of plant	727.39	33430.98**	373.46
No. of siliqua/ Secondary branch of plant	348.37	337521.31**	22726.82
Total No. of siliqua/ Plant	2082.54	545959.31**	25720.19
Seed yield/ Plant	0.63	797.64**	0.62
Siliqua length	0.01	0.79**	0.01
No. of seeds/ Siliqua	0.03	121.30**	0.13

Table 2: **Scaling test (Joint regression analysis) of different plant traits of *Brassica rapa.***

Traits	B	b=0	b=1	Wr±Vr	Wr-Vr
Plant Height	1.00±0.10	10.21*	-0.03^{NS}	12753.42**	357.07**
Seed Volume	0.97±0.07	13.89*	0.39^{NS}	8.31**	0.02^{NS}
1000 Seed Weight	0.81±0.15	5.44*	1.28^{NS}	10.40**	-0.53^{NS}
No. of siliqua/ Primary branch of plant	0.42±0.07	5.86*	8.26*	100170.70**	-32611.65^{NS}
No. of siliqua/ Secondary branch of plant	0.44 ±0.17	2.54*	3.20^{NS}	240770.83**	-79017.45**
Total No. of siliqua/ Plant	0.43±0.14	3.01*	3.98^{NS}	414613.75**	-537177.67**
Seed yield/ Plant	0.50±0.08	6.01*	5.95^{NS}	2371.93**	-718.44**
Siliquae length	0.98±0.08	11.57*	0.22^{NS}	23.91**	0.26^{NS}
No. of seeds/ Siliquae	0.95±0.11	8.45*	0.41^{NS}	438.88**	44.46**

seed volume (0.97 $\pm$ 0.07), plant height (1.00 $\pm$ 0.10), 1000 seed weight (0.81 $\pm$ 0.15), No. of siliqua/ primary branch of plant (0.42 $\pm$ 0.07), No. of siliqua/ secondary branch of plant (0.44 $\pm$ 0.17), total No. of siliqua/ plant (0.43 $\pm$ 0.14), seed yield/ plant (0.50 $\pm$ 0.08), siliqua length (0.98 $\pm$ 0.08) and No. of seeds/ siliquae (0.95 $\pm$ 0.11) deviating from zero revealed that this data was fit for genetic analysis.

Genetic analysis information was estimated through Wr/Vr graphical representation suggested by Hayman (1954) and Jinks (1954) from slope and position of regression line. These graphs are represented in Fig. 1 to Fig. 9.

Plant Height (cm)**:** The distribution of genotypic values in Fig.1 showed that BSA is farthest form the origin UAF-11 is near to origin as compared to others and Toria and TP-124-1 has moderate No. of dominant and recessive genes.

The components of variation relative magnitude for plant height is given in Table 3 as the value for H_1 (2921.674) is greater than D (1978.683) although D (1978.683) is greater than H_2 (189.591). The value of $\frac{1}{4}H_2/H_1$ (0.016) is less than 0.25. The value of (H1/D) ½ (1.215) is greater than 1. Direction of dominance h^2 (1076.680) is positive. The value of $(4DH_1)^{1/2}+F]/[(4DH_1)^{1/2}-F]$ (0.58) is greater than F (-1279.501). The value of narrow sense heritability is 0.982 which is 98.2%.

Seed Volume (cm³): The distribution of genotypic values in fig.2 showed that TP-124-1 is farthest form the origin while BSA is near to origin as compared to others and Toria and UAF-11 has moderate No. of dominant and recessive genes.

The components of variation relative magnitude for seed volume is given in Table 4 as the value for H_1 (7.707) is greater than D (4.384) although D (4.384) is greater than H_2. The value of $\frac{1}{4}H_2/H_1$ (0.017) is less than 0.25. The value of $(H1/D)^{1/2}$ (1.326) is greater than 1. Direction of dominance h^2 (2.310) is positive. The value of $[(4DH_1)^{1/2}+F]/[(4DH_1)^{1/2}-F]$ value (0.439) is greater than F (-4.532). The value of narrow sense heritability is 0.990 which is 99%.

1000 Seed weight**:** The distribution of genotypic values in fig.3 showed that TP-124-1 and UAF-11 are farthest from the origin at same position while BSA and Toria are near to origin at almost same positions. The components of variation relative magnitude for 1000 seed weight is given in Table 5 as the value for H_1 (2.82) is greater than D (1.307) although D (1.307) is greater than H_2 (0.503). The value of $\frac{1}{4}H_2/H_1$ (0.045) is less than 0.25. The value of (H1/D) ½ (1.469) is greater than 1. Direction of dominance h^2 (0.372) is positive. The value of $[(4DH_1)^{1/2}+F]$ / $[(4DH_1)^{1/2}-F]$ (0.485) is greater than F (-1.332). The value of narrow sense heritability is 0.951 which is 95.1%.

Table 3: **Components of variation in *Brassica rapa.***

Component	Plant Height Parameters±S.E.	Seed Volume Parameters±S.E.	1000 seed weight Parameters±S.E.
D (Additive effects)	1978.683±607.11	4.383±0.405	1.307±0.188
F (Frequency of dominant alleles)	-1279.501±488.20	-4.530±0.412	-1.332±0.190
H_1(Dominance effects)	2921.674±737.72	7.707±0.537	2.820±0.276
H_2 (Dominance effects)	189.591±187.93	0.523±0.140	0.503±0.116
h^2(Direction of dominance)	1076.680±447.84	2.310±0.294	0.372±0.100
$(H1/D)^{1/2}$	1.215	1.326	1.469
$\frac{1}{4}H_2/H_1$	0.016	0.017	0.045
h^2/H_2	5.679	4.420	0.740
$[(4DH_1)^{1/2}\pm F]/[(4DH_1)^{1/2}-F]$	0.580	0.439	0.485
h^2 ns (Narrow sense heritability)	0.982	0.990	0.951

Table 4: **Components of variation in *Brassica rapa.***

Component	No. of siliqua/ primary branches of plant Parameters±S.E.	No. of siliqua/ secondary branches of plant Parameters±S.E.	Total No. of siliqua/ plant Parameters±S.E.	Seed yield/ plant	Siliqua length	No. of Seeds/ Siliquae
D	6412.14±1298.93	76170.8±40.8	121021.8±2757.95	172.071±83.69	3.281±0.298	0.060±0.02
F	-14001.6±1919.43	-95799.8±45.5	-194345.9±34945	-316.945±113.58	-3.105±0.290	127.998±9.75
H_1	45483.0±3459.46	440945.8±97.8	752145.08±6875.5	1055.398±207.26	5.430±0.383	62.721±6.82
H_2	22310.3±2422.90	175165.8±61.3	310270.0±4415.95	495.199±141.97	0.128±0.059	131.779±9.89
h^2	76.9±142.27	16595.6±19.0	20435.3±1133.30	-0.218±0.05	1.446±0.198	45.072±5.78
$(H1/D)^{1/2}$	2.7	2.406	2.493	2.477	1.287	41.361±0.02
$\frac{1}{4}H_2/H_1$	0.1	0.099	0.103	0.117	0.006	1.015
h^2/H_2	0.003	0.095	0.066	0.000	11.295	0.086
$[(4DH_1)^{1/2}\pm F]/[(4DH_1)^{1/2}-F]$	0.4	0.586	0.513	0.458	0.462	0.918
h^2 ns	0.79	0.801	0.808	0.809	0.985	1.637

***No. of siliqua/ primary branches of plant*:** The distribution of genotypic values in fig.4 showed that BSA and Toria are farthest form the origin at almost same position while TP-124-1 is near to origin and UAF-11 is in middle. The components of variation relative magnitude for No. of siliqua/ Primary branches of plant is given in Table 6 as the value for H_1 (45483.003) and H_2 (22310.251) is greater than D (6412.135). The value of $¼H_2/H_1$ (0.123) is less than 0.25. The value of $(H_1/D)½$ (2.663) is greater than 1. Direction of dominance h^2 (76.923) is positive. The value of $[(4DH_1)½+F] / [(4DH_1)½-F]$ (0.418) is greater than F (-14001.557). The value of narrow sense heritability is 0.791 which is 79%.

***No. of siliqua/ secondary branch of plant*:** The distribution of genotypic values in fig.5 showed that UAF-11 is farthest form the origin and BSA and Toria are in middle while TP-124-1 is near to origin. The components of variation relative magnitude for No. of siliqua/ Secondary branches of plant is given in Table 7 as the value for H_1 (44945.811) and H_2 (175165.767) is greater than D (76170.769). The value of $¼H_2/H_1$ (0.103) is less than 0.25. The value of $(H_1/D)½$ (2. 43) is greater than 1. Direction of dominance h^2 (16595.566) is positive. The value of $[(4DH_1)½+F] / [(4DH_1)½-F]$ (0.586) is greater than F (-95799.776). The value of narrow sense heritability is 0.801 which is 80.1%.

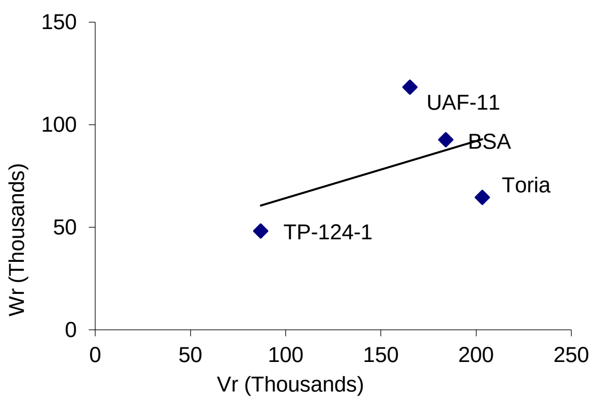

Figure 2: Graphical presentation of seed volume

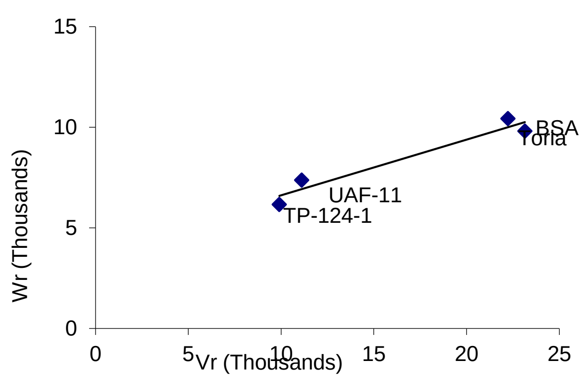

Figure 3: Graphical presentation of 1000 seed weight

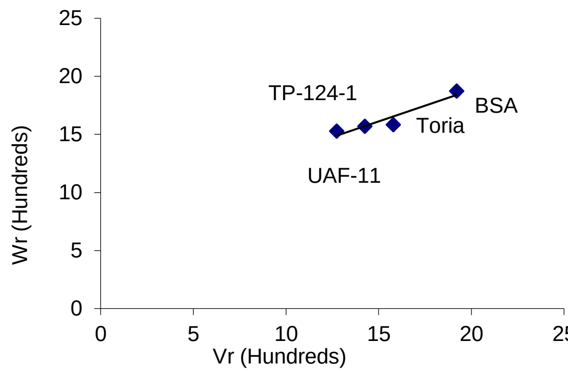

Figure 4: Graphical presentation of No. of siliqua/ primary branches of plant

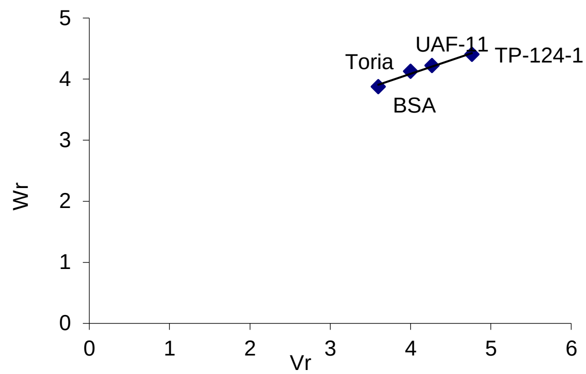

Figure 5: Graphical presentation of No. of siliqua/ secondary branches of plant

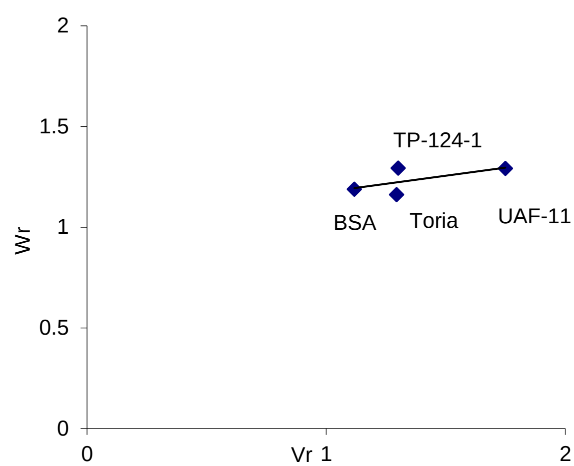

Figure 6: Graphical presentation of total No. of siliqua/ plant

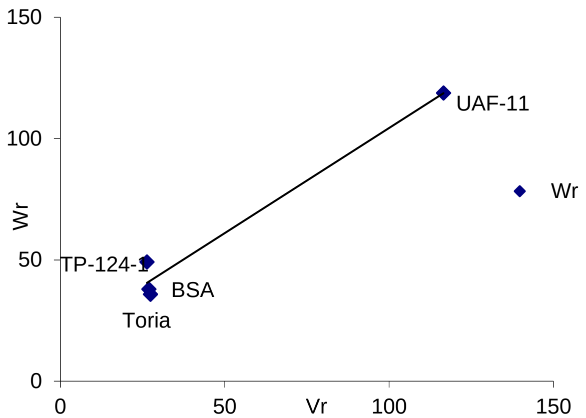

Figure 7: Graphical presentation of seed yield/ Plant

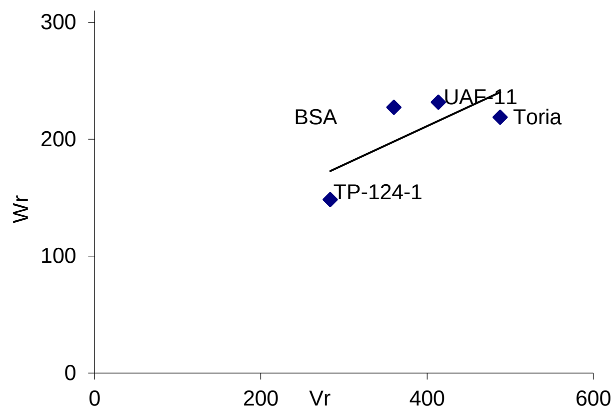

Figure 8: Graphical presentation of silique length

***Total No. of siliqua/ plant*:** The distribution of genotypic values in fig.6 showed that BSA is farthest form the origin while TP-124-1 is near to origin and UAF-11 are at middle position which means that they have intermediate dominant and recessive genes.

The components of variation relative magnitude for Total No. of siliqua/ Plant is given in Table 8 as the value for H_1 (752145.1) and H_2 (310270) is greater than D (121021.8). The value of $¼H_2/H_1$ (0.103) is less than 0.25. The value of $(H_1/D)½$ (2.493) is greater than 1. Direction of dominance h^2 (20435.324) is positive. The value of $[(4DH_1)½+F]$ / $[(4DH_1)½-F]$ (0.513) is greater than F (-194345.886). The value of narrow sense heritability is 0.808 which is 80.8%.

***Seed yield/ plant*:** The distribution of genotypic values in fig.9 showed that UAF-11 and Toria are farthest form the origin at almost same positions while TP-124-1 is near to origin and BSA is at middle position.

The components of variation relative magnitude for Seed yield/ Plant is given in Table 9 as the value for H_1 (1055.398) and H_2 (495.199) is greater than D (172.071). The value of $¼H_2/H_1$ (0.117) is less than 0.25. The value of (H_1/D) ½ (2.477) is greater than 1. Direction of dominance h^2 (-0.218) is negative. The value of $[(4DH_1)½+F]$ / $[(4DH_1)½-F]$ (0.458) is greater than F (-316.945). The value of narrow sense heritability is 0.809 which is 80.9%.

***Siliqua length*:** The distribution of genotypic values in fig.8 showed that TP-124-1 is farthest from the origin while BSA is near to origin as compared to other and Toria and UAF-11 are at middle position. The components of variation relative magnitude for siliqua length is given in Table 10 as the value for H_1 (5.430) is greater than D (3.281). The value of $¼H_2/H_1$ (0.006) is less than 0.25. The value of $(H_1/D)½$ (1.287) is greater than 1. Direction of dominance h^2 (1.446) is positive. The value of $[(4DH_1)½+F]$ / $[(4DH_1)½-F]$ (0.462) is greater than F (-3.105). The value of narrow sense heritability is 0.994 which is 99.4%.

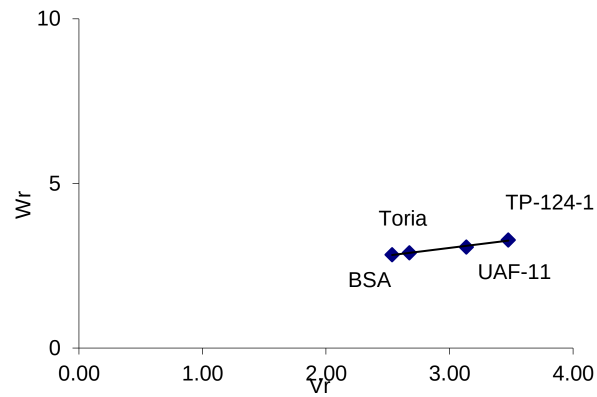

Figure 9: Graphical presentation of No. of seeds/siliquae

***No. of seeds/ siliqua*:** The distribution of genotypic values in fig.9 showed that UAF-11 is farthest form the origin while BSA, Toria and TP-124-1 are near to origin at almost same positions.

The components of variation relative magnitude for siliqua length is given in Table 11 as the value for H_1 (131.779) is greater than D (127.998) although value of D (127.998) is greater than H_2 (45.072). The value of $¼H_2/H_1$ (0.086) is less than 0.25. The value of $(H_1/D)½$ (1.015) is greater than 1. Direction of dominance h^2 (41.361) is positive. The value of F (62.721) is greater than $[(4DH_1)½+F]$ / $[(4DH_1)½-F]$ value (1.637). The value of narrow sense heritability is 0.87 which is 87%.

DISCUSSION

The goal of our study is to gather and develop information on genetics of different plant and seed yield related traits of *Brassica rapa*. Our study shows that UAF-11 is the best parent for Brassica rapa because it has the maximum dominant genes for almost all traits and can be utilized in future breeding efforts. As in graphical presentation the farthest genotype has maximum No. of recessive genes and

nearest genotype had maximum dominant genes and in middle genotypes has intermediate dominant and recessive genes. If interception of regression line on the covariance axis is above the origin then it indicated the presence of dominant type of gene action and if estimated regression line does not deviate significantly from unit slope, it indicated the absence of non-allelic interaction (epistasis). It was seen in all traits graphical distribution that in all traits covariance is above the origin and estimated regression line does not deviate significantly deviate from unit slope. From which it interpreted that partial dominance type of gene action is present among all of them and absence of non-allelic interaction is also interpreted.

It was interpreted from the graphical representations that for plant height that BSA has maximum no. of recessive genes while UAF-11 has maximum No. of dominant genes and Toria and TP-124-1 have intermediate No. of dominant and recessive genes. For seed volume, TP-124-1 has maximum no. of recessive genes while BSA has maximum No. of dominant genes and UAF-11 and Toria have intermediate No. of dominant and recessive genes. For 1000 seed weight, TP-124-1 and UAF-11 has maximum no. of recessive genes while Toria and BSA have maximum No. of dominant genes. For No. of siliquae/ primary branches of plant BSA and Toria have maximum No. of recessive genes while TP-124-1 has maximum dominant genes and UAF-11 has intermediate No. of recessive and dominant genes.

For No. of seeds/ secondary branches of plant, UAF-11 have maximum no. of recessive genes while TP-124-1 has maximum No. of dominant genes and BSA and Toria has intermediate No. of recessive and dominant genes. For total No. of siliquae/ plant, BSA has maximum no. of recessive genes while TP-124-1 has maximum No. of dominant genes and Toria and UAF-11 has intermediate No. of dominant and recessive genes. For seed yield/ plant, UAF-11 and Toria have maximum no. of recessive genes while TP-124-1 has maximum No. of dominant genes and BSA has intermediate No. of dominant and recessive genes. For silique length TP-124-1 has maximum no. of recessive genes while BSA has maximum No. of dominant genes and UAF-11 and Toria has intermediate No. of dominant and recessive genes. For No. of seeds/ silique UAF-11 has maximum recessive genes while BSA, Toria and TP-124-1 has maximum dominant genes. Similar types of results were also observed by Oghan *et al.*,2007, Pankaj *et al.*, 2008, Ahmed (2010), Sinhamahapatra *et al.*,(2010), Dar *et al.,(*2012), Rameeh (2012), Ahsan *et al.*, *(*2013), Ali *et al., (*2013), Nasim *et al.*, (2013) and Zada *et al.*, (2013).

In component of variation values, if value of D is higher than H_1 and H_2 then it means that it is controlled by dominant type of gene action and if it is less than H_2 it means some type of additive gene is controlled is present and if less than both then it means that additive genetic control is present. If the value of $¼H_2/H_1$ (0.003) is less than 0.25, it means maternal effect is present. Average degree of dominance was observed from $(H_1/D)½$ if, it is greater than 1, it indicated the presence of partial dominance type of gene action in controlling variation. Direction of dominance is indicated by $h^{2,}$ if it is positive it shows frequency of dominant genes towards better parents and if it is negative then it shows frequency of recessive genes towards better parents. If $[(4DH_1)½+F]/[(4DH_1)½-F]$ value is greater than F value, it indicated that No. of recessive genes are greater than No. of dominant genes and if it is less than F it mean No. of dominant genes are greater than No. of recessive genes.

From results it is observed that No. of siliqua/primary branches of plant,No. of siliqua/secondary branches of plant, Total No. of siliqua/plant, seed yield/plant and No. of seeds/silique was controlled by dominant gene action. Plant height, seed volume, 1000 seed weight, Siliqua length was controlled by dominant gene action and to some extend additive gene action was also present. Maternal effects were also present in all traits and direction of dominance was more frequent towards better parents in all traits except seed yield/ plant. No. of recessive genes were greater than No. of dominant genes in the parents in all traits except No. of seeds/siliqua. The high value of narrow sense heritability showed that selection on the basis of pall these traits can be helpful in future breeding programs. Similar types of results were also observed by Oghan *et al.*,2007, Pankaj *et al.*, 2008, Ahmed (2010), Sinhamahapatra *et al.,* (2010), Dar *et al.,(*2012), Rameeh (2012), Ahsan *et al.,(*2013); Ali *et al.,(*2013);Nasim *et al.,* (2013) and Zada *et al.,* (2013).

***Conclusion*:** UAF-11 was observed as best parent as it has maximum dominant genes for almost all traits. Partial dominant gene action was observed in all traits. Direction of dominance was more frequent towards better parents except seed yield per plant. No. of recessive genes were more than that of dominant genes except No. of seeds/siliqua.

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